

# **Visualization approaches for the comparison of hierarchies and the tasks for the comparison of biological taxonomies**

## **Guide for the Session with Experts**

**Please read this document before starting the session in which we will present a tool for the comparison of taxonomies**

### **Goal:**

To evaluate four visualization approaches for the comparison of hierarchies, which will be used in the context of the comparison of biological taxonomies, considering some of the common tasks that users carry out to make said comparison.

### **I. Introduction**

1. Our work consists in the visualization of the comparison of biological taxonomies.
2. In a previous work we identified 10 tasks that users perform when comparing taxonomies. Some of them are: identify splits, identify merges, identify moves, identify renamed taxa, identify new nodes added to the taxonomy and identify excluded nodes.
3. We developed a tool with the purpose of evaluating 4 classical visualization approaches when comparing hierarchies: a) edge drawing, b) matrix, c) animation and d) agglomeration.
4. The tool implements a representative subset of functions in order to carry out the identified tasks and sub-tasks.
5. In this exercise you will be asked to carry out some activities using the tool and we will record your answers and comments.

## **II. General description of the session**

1. Session has two parts:

Part 1: a tutorial about how to use the tool.

Part 2: The participants will carry out a set of tasks (exercises) using the tool. Before each exercise you will be given the respective instructions, we will tell you where to navigate and what information you should look for.

2. You will be asked to speak aloud as you resolve each exercise..
3. You will focus on the use of the tool and we will write your answers.
4. We will record the session for further reference.
5. For each approach we will use a different data set.
6. The exercise is intended to evaluate the approaches. It is not intended to evaluate participants.

### III. Guide for the use of tool.

1. Before the session you will receive a link that will give you access to the tool.
2. On top of the screen you will find 4 tabs, one for each approach: a) Edge drawing, b) Matrix, c) Animation, d) Agglomeration (see Figure 1).



Figure 1: One tab per approach.

3. **Common controls** to the 4 approaches.
  - On the top area of the window you can find 8 “on/off” buttons. Users use these buttons in order to perform the tasks. When turning on a button the corresponding differences and similarities will be shown. “All” button is intended to show all cases at once (see Figure 2):

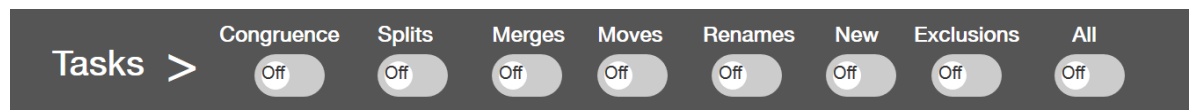


Figure 2: General controls bar. Buttons enable/disable the visualization of similarities and differences.

- By turning on the button you can visualize the type of similarity or difference between the two taxonomies. Examples: when turning Congruence “on” congruent taxa will be shown. When turning Splits “on” users can visualize all splits. When turning All “on” the system will simultaneously show all differences and similarities.
4. **Focus:** Users can focus on a taxon by selecting (that is, clicking) a taxon of their interest. Changes to the selected taxon will be displayed.
  5. **Edge drawing:**
    - a) Changes to a taxon will be shown by colored lines (edges). Each color represents a type of change as indicated in the General Controls bar.
    - b) Excluded taxa will be shown in red color (**red**).

- c) Included taxa will be shown in green color (**green**).
- d) Zoom in / zoom out can be performed by using the browser controls; that is, by pressing the *<ctrl> key and moving the mouse scroll wheel*.

6. **Matrix:**



- a) In the matrix representation changes are displayed by colored cells and colored texts.
- b) Excluded taxa will be shown in red color (**red**).
- c) Included taxa will be shown in green color (**green**).
- d) Zoom in / Zoom out, there are two alternatives:
  - by using the browser controls; that is, by pressing the *<ctrl> key and moving the mouse scroll wheel*.
  - Key I (zoom in) y key O (zoom out). Click the matrix and then press either key I or key O.
- e) To move the matrix in the window, you can either:
  - use the scroll bars, or
  - Drag the matrix by clicking on it and then moving the mouse.

## 7. Animation:

- a) Changes are animated.
- b) Specific controls for animation:
  - Besides the general controls explained above, animation has specific controls as shown in Figure 3.



Figure 3: Controls for animation.

- “Reset” button: it turns the visualization to the initial state, and all buttons are turned “Off”.
  - “Play” () it is to start the animation. Once the animation begins, the pause button appears () in case you want to pause the animation.
  - Right after the “play” button you can find the speed bar.
  - “By Taxon” button works as follows:
    - *Off*: all selected types of change are animated simultaneously.
    - *On*: all selected types of change are animated one by one. For instance, if “Splits” is “On” and there are 2 splits, the animation presents the first split and when its animation is over it starts to present animation for the second split.
- f) Excluded taxa will be shown in red color (**red**).
  - g) Included taxa will be shown in green color (**green**).
  - h) Zoom in / Zoom out, there are two alternatives:
    - by using the browser controls; that is, by pressing the *<ctrl>* key and moving the mouse scroll wheel.
    - Key I (zoom in) y key O (zoom out). Click the visualization and then press either key I or key O.
  - i) To move the visualization in the window, you can either:
    - use the scroll bars, or
    - drag the visualization by clicking on it and then moving the mouse.

## 8. Agglomeration:

- a) Taxonomies are agglomerated (merged) into one structure.
- b) Light gray taxa correspond to the reference taxonomy (for instance, an older version of the taxonomy) and dark gray taxa correspond to the compared taxonomy (for instance, the newer version of the taxonomy). To avoid node repetition within the structure, common ancestors are presented in light gray.
- c) Excluded taxa will be shown in red color (**red**).
- d) Included taxa will be shown in green color (**green**).
- e) Color is used to relate taxa within the reference taxonomy to taxa within the compared taxonomy. Same color is used with different brightness to show relationships between the two taxonomies. For instance (see Figure 4) light colors correspond to the reference taxonomy and dark colors correspond to the compared taxonomy.



Figure 4: Color codes for agglomeration.

j) Zoom in / Zoom out, there are two alternatives:

- by using the browser controls; that is, by pressing the *<ctrl> key and moving the mouse scroll wheel.*
- Key I (zoom in) y key O (zoom out). Click the visualization and then press either key I or key O.

k) To move the visualization in the window, you can either:

- use the scroll bars, or
- drag the visualization by clicking on it and then moving the mouse.